

information" in essence means "sequenced gene information" or "genetic sequences." In particular, the recitation "gene arrangement information" means "sequenced gene information" or "genetic sequences." Accordingly, dependent claim 2 depending from claim 1, is amended into independent form and further amended by deleting the recitation "clarified."

Withdrawal of the rejection of claims 1-7 under 35 USC 112, second paragraph, is respectfully requested.

SPECIFICATION

Consistent with the above rationale regarding the term "clarified" in claim 1 the specification, page 1, the paragraph beginning at line 12, is amended to improve form and clarity.

CLAIMED INVENTION

Dependent claim 2 depending from claim 1, is amended into independent form. Claim 2 is further amended to emphasize the patentably distinguishing features of the present invention. Independent claims 8 and 9 are amended consistent with claim 2.

In contrast to Attwood and Kawanishi, the present invention as recited in amended dependent claims 2, 8 and 9, using the recitation of claim 2 as an example, comprises:

... motif extraction range designating means for an operator interactively designating on a display screen a motif extraction range in the input gene arrangement information and extracting a genetic motif within the designated extraction range from the input gene arrangement information;

gene arrangement information retrieving means for retrieving, based on the motif extracted from the input gene arrangement information, gene arrangement information including the extracted motif, from said gene arrangement information storing means; and

gene arrangement information adding means for adding the retrieved extracted-motif-based gene arrangement information to the input gene arrangement information (emphasis added).

A benefit of the invention is to reutilize a motif extracted from an input gene information to be sequenced by adding to the input gene sequence a gene sequence retrieved from existing gene sequences that includes the extracted motif of the input gene sequence. Such reutilization of a motif within an input gene information improves the motif extracting efficiency for determining functions and structures of genes.

35 USC 102 and 103 REJECTIONS**PRIOR ART****Attwood**

Claims 1, 3 and 5-9 are rejected under 35 USC 102(b) over Attwood. Attwood discloses a pattern recognition method for analysis of a novel genetic sequence. In page 418, left column, Attwood discloses the following method: extracting motifs from sequence alignments and using the extracted motifs to make independent scans of the database to determine if any additional sequences have matched all the extracted motifs. If this is true, information from the new matching sequences is added to the initial motifs, and the database is searched again. The Sequence information is thus augmented through iterative database scanning.

The Examiner appears to assert that Attwood's augmentation is similar to the present invention's claimed feature: "adding the retrieved extracted-motif-based gene arrangement information to the input gene arrangement information." However, Attwood, page 418, left column, discloses that the new sequences are added to the initial motifs. In particular, Attwood in page 418, discloses that sequence information is augmented (i.e., supplemented, or added to) through iterative database scanning. Therefore, the present invention's claimed feature is patentably distinguishing from Attwood, because in the present invention the object (target) to which the retrieved information (retrieved gene arrangement information) is added, is not the database (existing gene arrangement information) but "the input gene arrangement information" to be sequenced. Accordingly, because the object (target) to which the retrieved gene arrangement information is added differs between Attwood and the present invention, Attwood does not disclose or suggest: "processing/function of extracting a genetic motif within the designated extraction range from the input gene arrangement information ... and adding ... retrieved extracted-motif-based gene arrangement information to the input gene arrangement information" (claim 2). A benefit of the invention is to reutilize a motif extracted from an input gene information to be sequenced, by adding to the input gene sequence a gene sequence retrieved from existing gene sequences that includes the extracted motif of the input gene sequence, thereby improving a motif extracting efficiency for determining functions and structures of genes.

Kawanishi

The Office Action on page 4 indicates that claims 1-9 are rejected under 35 USC 103 (a) over Attwood and Kawanishi. However, the rejections only discuss claims 2-4, appearing that

the Examiner is only rejecting claims 2-4 over Attwood and Kawanishi.

The Examiner acknowledges that Attwood does not teach the means for designating a motif range, and relies on Kawanishi for this claimed features. Kawanishi discloses extracting a genetic motif from genetic sequences based upon weighting of each genetic sequence and a score of the weightings (column 4, lines 4-21). In particular, the Examiner appears to assert that Kawanishi's method to extract a motif site having a regularity of the distinctive feature in the genetic sequences, based on calculated score (column 4, lines 4-35), is similar to the present invention's claimed feature: "designating ... a motif extraction range." However, Kawanishi's technique merely automatically designates the motif extraction range in previously sequenced genes based upon the calculated weightings of these previously sequenced genes, and does not relate to "interactively designating ... the motif extraction range in the input gene arrangement information" (claim 2). More particularly, in contrast to Kawanishi, the present invention as recited in amended claim 2, provides "an operator interactively designating on a display screen a motif extraction range in the input gene arrangement information." Because the technical idea of allowing manually designating, such as narrowing, a motif extraction range is not disclosed in Kawanishi or Attwood, these relied upon references do not provide a suggestion to anticipate or render obvious the present invention.

Therefore, another benefit of the present invention is that the designation of the motif extraction range in an input gene sequence is possible, and also the designation of the extracted range is possible on a screen interactively. Then, if the designation of the motif extraction range is possible interactively, because the operation becomes easy, the operator can concentrate on sequencing function or structure of a gene, thereby improving the motif extraction efficiency.

CONCLUSION

Dependent claims 3-7 (depending, either directly or indirectly, from claim 2) recite patentably distinguishing features of their own, and further, are at least patentably distinguishing due to their dependencies from independent claim 2.


In view of the amendments and remarks presented above, it is respectfully submitted that the application is in condition for allowance, and withdrawal of the rejection of claims 2-9 and allowance of claims 2-9 is respectfully requested.

Attached hereto is a marked-up version of the changes made to the claims by the current amendment. The attached page is captioned "**VERSION WITH MARKINGS TO SHOW CHANGES MADE.**"

If there are any formal matters remaining after this response, the Examiner is requested to telephone the undersigned to attend to these matters.

Respectfully submitted,
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VERSION WITH MARKINGS TO SHOW CHANGES MADE**IN THE ABSTRACT**

The **ABSTRACT** is replaced as follows.

--A genetic motif is extracted from at least one piece of input gene arrangement information, and[, based on the extracted motif, gene arrangement information including[, as a part thereof,] the motif as a part thereof is retrieved from previously [clarified]sequenced gene [arrangement] information. The gene arrangement information as retrieved is added to the input gene arrangement information, to thereby improve a genetic motif extracting efficiency.--

IN THE SPECIFICATION

The paragraph beginning at page 1, line 12, starting with "Recent progress" is **REPLACED** as follows:

--Recent progress of genetic engineering has brought rapid progress of a technique for determining a gene arrangement such as expressed by a DNA sequence and/or an amino acid sequence. Further, the genome project is being conducted worldwide so as to clarify all gene arrangements of specific organisms (i.e., to sequence or identify gene information), for various species including human beings. As such, databases of gene arrangement information have [been] increased explosively, so as to effectively utilize those previously clarified gene arrangement information (sequenced gene information or genetic sequences).--

IN THE CLAIMS

Claim 1 is **CANCELLED**.

Claims 2-6 and 8-9 are **AMENDED** as follows.

Recitation of all pending claims is provided for reference convenience.

1. (CANCELLED)

2. (ONCE AMENDED) A genetic motif extracting and processing apparatus [according to claim 1, further] comprising:

gene arrangement information storing means for storing gene arrangement information;

gene arrangement information inputting means for inputting at least one piece of gene arrangement information;

motif extraction range designating means for an operator interactively designating on a display screen [designating, in the gene arrangement information input by the gene arrangement

information inputting means,] a motif extraction range in the input gene arrangement information and [for the motif extracting means,

wherein the motif] extracting [means extracts] a genetic motif [from] within the designated extraction range [designated by the motif extraction range designating means] from the input gene arrangement information;

gene arrangement information retrieving means for retrieving, based on the motif extracted from the input gene arrangement information, gene arrangement information including the extracted motif, from said gene arrangement information storing means; and

gene arrangement information adding means for adding the retrieved extracted-motif-based gene arrangement information to the input gene arrangement information.

3. (ONCE AMENDED) A genetic motif extracting and processing apparatus according to claim [1]2, further comprising gene arrangement information editing means for editing the gene arrangement information.

4. (ONCE AMENDED) A genetic motif extracting and processing apparatus according to claim [1]2, further comprising motif editing means for editing the motif extracted by the motif extracting means.

5. (ONCE AMENDED) A genetic motif extracting and processing apparatus according to claim [1]2, further comprising alignment means for alignment-processing a plurality of gene arrangement information input by the gene arrangement information inputting means.

6. (ONCE AMENDED) A genetic motif extracting and processing apparatus according to claim [1]2, further comprising:
motif storing means for storing motifs; and
motif registering means for registering the motif extracted by the motif extracting means into said motif storing means.

7. A genetic motif extracting and processing apparatus according to claim 6, further comprising motif displaying means for displaying at least one motif from those motifs registered in the motif storing means.

8. (ONCE AMENDED) A genetic motif extracting and processing method

comprising:

[a gene arrangement information inputting process for] inputting at least one piece of gene arrangement information;

designating interactively on a display screen a motif extraction range in the input gene arrangement information;

[a motif extracting process for] extracting a genetic motif within the designated motif extraction range from the input gene arrangement information [input by said gene arrangement information inputting process];

[a gene arrangement information retrieving process for] retrieving, based on the extracted motif from the input gene arrangement information [extracted by said motif extracting process], gene arrangement information including [said] the extracted motif [as a part thereof], from a gene arrangement information database; and

[a gene arrangement information adding process for] adding[,] the retrieved extracted-motif-based gene arrangement information [retrieved by said gene arrangement information retrieving process,] to the input gene arrangement information [input by the gene arrangement information inputting process].

9. (ONCE AMENDED) A recording medium recorded with a genetic motif extracting and processing program [for] realizing a process of:

[a gene arrangement information inputting function for] inputting at least one piece of gene arrangement information;

designating interactively on a display screen a motif extraction range in the input gene arrangement information;

[a motif extracting function for] extracting a genetic motif within the designated motif extraction range from the input gene arrangement information [input by said gene arrangement information inputting function];

[a gene arrangement information retrieving function for] retrieving, based on the extracted motif from the input gene arrangement information [extracted by said motif extracting function], gene arrangement information including [said] the extracted motif [as a part thereof], from a gene arrangement information database; and

[a gene arrangement information adding function for] adding[,] the retrieved extracted-motif-based gene arrangement information [retrieved by said gene arrangement information retrieving function,] to the input gene arrangement information [input by the gene arrangement information inputting function].